

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gregory Plowman  
Douglas Clary
- (ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
Alk-7 RELATED DISORDERS
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Lyon & Lyon  
(B) STREET: 633 West Fifth Street  
Suite 4700  
(C) CITY: Los Angeles  
(D) STATE: California  
(E) COUNTRY: U.S.A.  
(F) ZIP: 90071-2066
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0  
(D) SOFTWARE: FastSEQ for Windows 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: To be assigned  
(B) FILING DATE: Filed herewith  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 60/044,428  
(B) FILING DATE: April 28, 1997
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Warburg, Richard J.  
(B) REGISTRATION NUMBER: 32,327  
(C) REFERENCE/DOCKET NUMBER: 234/118
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (213) 489-1600  
(B) TELEFAX: (213) 955-0440  
(C) TELEX: 67-3510

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1793 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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CGGCCACACT GACTAGAGCC AACC GCGCAC TTCAAAGGG TGTGGTGCC GCGCTCCCTT 60
CCCGCGGCC GGAACCTCA AAGCGGGCCG TGCTGCCCCG GCTGCCTCGC TCTGCTCTGG 120
GGCCTCGCAG CCGCGGCGCG GCCGCCTGGT GGCGATGACC CGGGCGCTCT GCTCAGCGCT 180
CCGCCAGGCT CTCCTGCTGC TCGCAGCGGC CGCCGAGCTC TCGCCAGGAC TGAAGTGTGT 240
ATGTCTTTTG TGTGATTCTT CAAACTTTAC CTGCCAAACA GAAGGAGCAT GTTGGGCATC 300
AGTCATGCTA ACCAATGGAA AAGAGCAGGT GATCAAATCC TGTGTCTCCC TTCCAGAACT 360
GAATGCTCAA GTCTTCTGTC ATAGTTCCAA CAATGTTACC AAAACCGAAT GCTGCTTCAC 420
AGATTTTTTG AACAACATAA CACTGCACCT TCCAACAGCA TCACCAAATG CCCCAAAAC 480
TGGACCCATG GAGCTGGCCA TCATTATTAC TGTGCCTGTT TGCCTCCTGT CCATAGCTGC 540
GATGCTGACA GTATGGGCAT GCCAGGGTCG ACAGTGCTCC TACAGGAAGA AAAAGAGACC 600
AAATGTGGAG GAACCACTCT CTGAGTGCAA TCTGGTAAAT GCTGGAAAAA CTCTGAAAGA 660
TCTGATTTAT GATGTGACCG CCTCTGGATC TGGCTCTGGT CTACCTCTGT TGGTTCAAAG 720
GACAATTGCA AGGACGATTG TGCTTCAGGA AATAGTAGGA AAAGGTAGAT TTGGTGAGGT 780
GTGGCATGAT AGATGGTGTG GGAAGATGT GGCTGTGAAA ATATTCTCCT CCAGAGATGA 840
AAGATCTTGG TTTCGTGAGG CAGAAATTA CCAGACGGTC ATGCTGCGAC ATGAAAACAT 900
CCTTGTTTTT ATTGCTGCTG ACAACAAAGA TAATGGAAC TGGACTCAAC TTTGGCTGGT 960
ATCTGAATAT CATGAACAGG GCTCCTTATA TGAATTTTG AATAGAAATA TAGTGACCGT 1020
GGCTGGAATG ATCAAGCTGG CGCTCTCAAT TGCTAGTGGT CTGGCACACC TTCATATGGA 1080
GATTGTTGGT ACACAAGGTA AACCTGCTAT TGCTCATCGA GACATAAAAT CAAAGAATAT 1140
CTTAGTGAAA AAGTGTGAAA CTTGTGCCAT AGCGGACTTA GGGTTGGCTG TGAAGCATGA 1200
TTCAATACTG AACACTATCG ACATACCTCA GAATCCTAAA GTGGGAACCA AGAGGTATAT 1260
GGCTCCTGAA ATGCTTGATG ATACAATGAA TGTGAATATC TTTGAGTCCT TCAAACGAGC 1320
TGACATCTAT TCTGTTGGTC TGGTTTACTG GGAATAGGCC CGGAGGTGTT CAGTCGGAGG 1380
AATTGTTGAG GAGTACCAAT TGCCTTATTA TGACATGGTG CCTTCAGATC CCTCGATAGA 1440
GGAAATGAGA AAGGTTGTTT GTGACCAGAA GTTTCGACCA AGTATCCCAA ACCAGTGGCA 1500
AAGTTGTGAA GCACTCCGAG TCATGGGGAG AATAATGCGT GAGTGTGGT ATGCCAACGG 1560
AGCGGCCCGC CTAACCTGCTC TTCGTATTAA GAAGACTATA TCTCAACTTT GTGTCAAAGA 1620
AGACTGCAAA GCCTAATGAT GATAATTATG TTAATAAGAA ATCTCTCATA GCTTTCTTTT 1680
CCATTTTCCC CTTTATGTGA ATGTTTTTGC CATTTTTTTT TTGTTCTACC TCAAAGATAA 1740
GACAGTACAG TATTTAAGTG CCCATAAGGC AGCATGAAAA GATAACTCTA AAG 1793
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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Met Thr Arg Ala Leu Cys Ser Ala Leu Arg Gln Ala Leu Leu Leu Leu
1           5           10           15
Ala Ala Ala Ala Glu Leu Ser Pro Gly Leu Lys Cys Val Cys Leu Leu
20           25           30
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Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala Cys Trp Ala  
 35 40 45  
 Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ile Lys Ser Cys Val  
 50 55 60  
 Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser Ser Asn Asn  
 65 70 75 80  
 Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn Asn Ile Thr  
 85 90 95  
 Leu His Leu Pro Thr Ala Ser Pro Asn Ala Pro Lys Leu Gly Pro Met  
 100 105 110  
 Glu Leu Ala Ile Ile Ile Thr Val Pro Val Cys Leu Leu Ser Ile Ala  
 115 120 125  
 Ala Met Leu Thr Val Trp Ala Cys Gln Gly Arg Gln Cys Ser Tyr Arg  
 130 135 140  
 Lys Lys Lys Arg Pro Asn Val Glu Glu Pro Leu Ser Glu Cys Asn Leu  
 145 150 155 160  
 Val Asn Ala Gly Lys Thr Leu Lys Asp Leu Ile Tyr Asp Val Thr Ala  
 165 170 175  
 Ser Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala  
 180 185 190  
 Arg Thr Ile Val Leu Gln Glu Ile Val Gly Lys Gly Arg Phe Gly Glu  
 195 200 205  
 Val Trp His Gly Arg Trp Cys Gly Glu Asp Val Ala Val Lys Ile Phe  
 210 215 220  
 Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln  
 225 230 235 240  
 Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp  
 245 250 255  
 Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Glu Tyr  
 260 265 270  
 His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn Ile Val Thr  
 275 280 285  
 Val Ala Gly Met Ile Lys Leu Ala Leu Ser Ile Ala Ser Gly Leu Ala  
 290 295 300  
 His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala  
 305 310 315 320  
 His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys Cys Glu Thr  
 325 330 335  
 Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp Ser Ile Leu  
 340 345 350  
 Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr Lys Arg Tyr  
 355 360 365

Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn Ile Phe Glu  
 370 375 380  
 Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val Tyr Trp Glu  
 385 390 395 400  
 Ile Ala Arg Arg Cys Ser Val Gly Gly Ile Val Glu Glu Tyr Gln Leu  
 405 410 415  
 Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg  
 420 425 430  
 Lys Val Val Cys Asp Gln Lys Phe Arg Pro Ser Ile Pro Asn Gln Trp  
 435 440 445  
 Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met Arg Glu Cys  
 450 455 460  
 Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys  
 465 470 475 480  
 Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala  
 485 490

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: "Xaa" in positions 6 and 7 stand for an unspecified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

His Arg Asp Leu Lys Xaa Xaa Asn  
 1 5

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: The letter "R" stands for A or G.  
The letter "N" stands for Inosine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
GARRAGTNG CNGTNAARRT NTT

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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "R" stands for A or G.  
The letter "N" stands for Inosine.  
The letter "K" stands for G or T.  
The letter "M" stands for A or C.  
The letter "Y" stands for C or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
TTRATRTCNC KRTGNGMNAT NGMNGGYTT

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(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in position 2 stands for Lys or  
Glu. "Xaa" in position 7 stands for  
Val or Ile.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
Glu Xaa Val Ala Val Lys Xaa Phe  
1 5

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in position 3 stands for Ala or Ser. "Xaa" in position 5 stands for Ala or Ser.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Lys Pro Xaa Ile Xaa His Arg Asp Ile Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AACTTTGGCT GGTATCTGAA TATC 24

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCTTGTGTAC CAACAATCTC CATA 24

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCCAGAGAT GAGAGATCTT GG 22

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
TTCCAGCCAC GGTCACTATG TT

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(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Tyr Arg Lys Lys Lys Arg Pro Asn Val Glu Glu Pro Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CTTCGAAAGC TTGAAATCGG TACCATCGAT TCTAGAGTTA ACTTCGAA

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(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCTAGAACG CGTTAAGGCG CGCCAATATC GATGAATTCT TCGAAGC

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